

B3 8. (Once amended) The reagent of claim 1 wherein the affinity label is selected from the group consisting of a 1,2-diol, glutathione, maltose, a nitrilotriacetic acid group, and an oligohistidine.

B4 13. (Once amended) The reagent of claim 1 wherein PRG is selected from the groups consisting of a amine reactive pentafluorophenyl ester group, an amine reactive N-hydroxy succinimide ester group, sulfonyl halide, isocyanate, isothiocyanate, active ester, tetrafluorophenyl ester, an acid halide, and an acid anhydride; a homoserine lactone reactive primary amine group, and a carboxylic acid reactive amine, alcohols or 2,3,5,6-tetrafluorophenyl trifluoroacetate.

15. (Once amended) The reagent of claim 1 wherein PRG is a substrate for an enzyme a deficiency of which is associated with a birth defect.

16. (Once amended) The reagent of claim 1 wherein PRG is a substrate for an enzyme a deficiency of which is associated with a lysosomal storage disease.

B5 17. (Once amended) The reagent of claim 1 wherein PRG is a substrate for acid sphingomyelinase, galactocerebroside β -galactosidase, β -galactosidase, acetyl- α -D-glucosaminidase, heparan sulfamidase, acetyl-CoA- α -D-glucosaminide N-acetyltransferase or N-acetylglucosamine-6-sulfatase.

18. (Once amended) The reagent of claim 1 wherein at least one of B¹ or B² is CO-NR' or CS-NR.

Amendments to the Specification

Please replace the second paragraph on page 1, under the heading CROSS-REFERENCE TO RELATED APPLICATIONS, with the following.

B6 This application is a division of U.S. patent application serial no. 09/383,062, filed August 25, 1999, which takes priority under 35 U.S.C. §119(e) from U.S. provisional application serial

no. 60/097,788, filed August 25, 1998, and serial no. 60/099,113, filed September 3, 1998, all of which are incorporated in their entirety by reference herein.

Page 2, second full paragraph

At present no protein analytical technology approaches the throughput and level of automation of genomic technology. The most common implementation of proteome analysis is based on the separation of complex protein samples most commonly by two-dimensional gel electrophoresis (2DE) and the subsequent sequential identification of the separated protein species (Ducret et al., 1998; Garrels et al., 1997; Link et al., 1997; Shevchenko et al., 1996; Gygi et al. 1999; Boucherie et al., 1996). This approach has been revolutionized by the development of powerful mass spectrometric techniques and the development of computer algorithms which correlate protein and peptide mass spectral data with sequence databases and thus rapidly and conclusively identify proteins (Eng et al., 1994; Mann and Wilm, 1994; Yates et al., 1995). This technology has reached a level of sensitivity which now permits the identification of essentially any protein which is detectable by conventional protein staining methods including silver staining (Figeys and Aebersold, 1998; Figeys et al., 1996; Figeys et al., 1997; Shevchenko et al., 1996). However, the sequential manner in which samples are processed limits the sample throughput, the most sensitive methods have been difficult to automate and low abundance proteins, such as regulatory proteins, escape detection without prior enrichment, thus effectively limiting the dynamic range of the technique. In the 2DE/(MS)ⁿ method, proteins are quantified by densitometry of stained spots in the 2DE gels.

[Paragraph bridging pages 2 and 3]

The development of methods and instrumentation for automated, data-dependent electrospray ionization (ESI) tandem mass spectrometry (MSⁿ) in conjunction with microcapillary liquid chromatography (μ LC) and database searching has significantly increased the sensitivity and speed of the identification of gel-separated proteins. As an alternative to the 2DE/MSⁿ approach to proteome analysis, the direct analysis by tandem mass spectrometry of peptide mixtures generated by the digestion of complex protein mixtures has been proposed (Dongre et al., 1997). μ LC-MS/MS has also been used successfully for the large-scale identification of individual proteins directly from mixtures without gel electrophoretic separation (Link et al., 1999; Opitke et al., 1997). While these approaches dramatically accelerate protein identification, the quantities of the analyzed proteins cannot be easily determined, and these methods have not been shown to substantially alleviate the dynamic range problem also encountered by the

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2DE/MS/MS approach. Therefore, low abundance proteins in complex samples are also difficult to analyze by the μ LC/MS/MS method without their prior enrichment.

Page 5, second full paragraph:

In general, the affinity labeled protein reactive reagents of this invention have three portions: an affinity label (A) covalently linked to a protein reactive group (PRG) through a linker group (L):

A-L-PRG

The linker may be differentially isotopically labeled, e.g., by substitution of one or more atoms in the linker with a stable isotope thereof. For example, hydrogens can be substituted with deuteriums or ^{12}C with ^{13}C .

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[Paragraph bridging pages 5 and 6]

The affinity label A functions as a molecular handle that selectively binds covalently or non-covalently, to a capture reagent (CR). Binding to CR facilitates isolation of peptides, substrates or reaction products tagged or labeled with A. In specific embodiments, A is a streptavidin or avidin. After affinity isolation of affinity tagged materials, some of which may be isotopically labeled, the interaction between A and the capture reagent is disrupted or broken to allow MS analysis of the isolated materials. The affinity label may be displaced from the capture reagent by addition of displacing ligand, which may be free A or a derivative of A, or by changing solvent (e.g., solvent type or pH) or temperature conditions or the linker may be cleaved chemically, enzymatically, thermally or photochemically to release the isolated materials for MS analysis.

Paragraph bridging pages 8 and 9

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Quantitative relative amounts of proteins in one or more different samples containing protein mixtures (e.g., biological fluids, cell or tissue lysates, etc.) can be determined using chemically identical, affinity tagged and differentially isotopically labeled reagents to affinity tag and differentially isotopically label proteins in the different samples. In this method, each sample to be compared is treated with a different isotopically labeled reagent to tag certain proteins therein with the affinity label. The treated samples are then combined, preferably in equal amounts, and the proteins in the combined sample are enzymatically digested, if necessary, to generate peptides. Some of the peptides are affinity tagged and in addition tagged peptides originating from different samples are differentially isotopically labeled. As

described above, affinity labeled peptides are isolated, released from the capture reagent and analyzed by (LC/MS). Peptides characteristic of their protein origin are sequenced using MSⁿ techniques allowing identification of proteins in the samples. The relative amounts of a given protein in each sample is determined by comparing relative abundance of the ions generated from any differentially labeled peptides originating from that protein. The method can be used to assess relative amounts of known proteins in different samples. Further, since the method does not require any prior knowledge of the type of proteins that may be present in the samples, it can be used to identify proteins which are present at different levels in the samples examined. More specifically, the method can be applied to screen for and identify proteins which exhibit differential expression in cells, tissue or biological fluids. It is also possible to determine the absolute amounts of specific proteins in a complex mixture. In this case, a known amount of internal standard, one for each specific protein in the mixture to be quantified, is added to the sample to be analyzed. The internal standard is an affinity tagged peptide that is identical in chemical structure to the affinity tagged peptide to be quantified except that the internal standard is differentially isotopically labeled, either in the peptide or in the affinity tag portion, to distinguish it from the affinity tagged peptide to be quantified. The internal standard can be provided in the sample to be analyzed in other ways. For example, a specific protein or set of proteins can be chemically tagged with an isotopically-labeled affinity tagging reagent. A known amount of this material can be added to the sample to be analyzed. Alternatively, a specific protein or set of proteins may be labeled with heavy atom isotopes and then derivatized with an affinity tagging reagent.

Please insert the following at page 11 of the specification before the heading "DETAILED DESCRIPTION OF THE INVENTION."

BRIEF DESCRIPTION OF THE FIGURES

Figure 1 is a standard curve generated with a cysteine-biotinylated peptide and quantitated by stable isotope dilution. A) Zoom-scan from an ion-trap mass spectrometer showing a 4 amu isotope distribution for the $[M+2H]^{2+}$ ions of the peptide modified with the isotopically light (1457.9 u) and heavy (1461.8) biotinylating reagents. The ratio (d0/d8) was 4.54. B) Curve generated from the analysis of isotope ratios from zoom-scans of 5 different concentrations of d0-labeled peptide measured in the presence of a known amount of peptide labeled with the isotopically heavy reagent.

Figure 2 is a tandem mass spectrum of a cysteine-modified peptide from α -lactalbumin.

Figure 3 shows a mass spectrum for a single differentially labeled peptide pair. Figure 3A shows four pairs of peptide ions characterized by the mass differential encoded in the affinity tagged reagent. Figure 3B shows an expanded view of the mass spectrum around one ion pair. Figure 3C shows the reconstructed ion chromatograms for each peak of the pair in Figure 2.

Figure 4A shows the CID spectrum for one of the peaks of one of the peptides analyzed in Fig. 3. Figure 4B shows the result of database searching the CID spectrum of Figure 4A.

Figure 5A shows the method by which yeast group on ethanol by converting ethanol into acetaldehyde which enters the TCA cycle. Figure 5B shows the mass spectrum for ADH1 gene expression for yeast grown on ethanol or sugar. Figure 5B shows the mass spectrum for ADH2 yeast gene expression for yeast grown on either ethanol or galactose.

Figures 6A – 6C represent the clinical analysis of patient samples for GM1 and SFB. See “Clinical Enzymology Assays.”

Figure 7 is a schematic representation of the automated LC-MS/MS system.

Figure 8 is a schematic representation of the SPE⁶-CE-MS/MS system.

Paragraph bridging pages 11 and 12

Suitable affinity tags bind selectively either covalently or non-covalently and with high affinity to a capture reagent (CR). The CR-A interaction or bond should remain intact after extensive and multiple washings with a variety of solutions to remove non-specifically bound components. The affinity tag binds minimally or preferably not at all to components in the assay system, except CR, and does not significantly bind to surfaces of reaction vessels. Any non-specific interaction of the affinity tag with other components or surfaces should be disrupted by multiple washes that leave CR-A intact. Further, it must be possible to disrupt the interaction of A and CR to release peptides, substrates or reaction products, for example, by addition of a displacing ligand or by changing the temperature or solvent conditions. Preferably, neither CR nor A react chemically with other components in the assay system and both groups should be

chemically stable over the time period of an assay or experiment. The affinity tag preferably does not undergo peptide-like fragmentation during (MS)ⁿ analysis. The affinity label is preferably soluble in the sample liquid to be analyzed and the CR should remain soluble in the sample liquid even though attached to an insoluble resin such as Agarose. In the case of CR the term soluble means that CR is sufficiently hydrated or otherwise solvated such that it functions properly for binding to A. CR or CR-containing conjugates should not be present in the sample to be analyzed, except when added to capture A.

Page 12, first full paragraph:

Examples of A and CR pairs include:

d-biotin or structurally modified biotin-based reagents, including d-iminobiotin, which bind to proteins of avidin/streptavidin, which may, for example, be used in the forms of streptavidin-Agarose, oligomeric-avidin-Agarose, or monomeric-avidin-Agarose;

any 1,2-diol, such as 1,2-dihydroxyethane (HO-CH₂-CH₂-OH), and other 1,2-dihydroxyalkanes including those of cyclic alkanes, e.g., 1,2-dihydroxycyclohexane which bind to an alkyl or aryl boronic acid or boronic acid esters, such as phenyl-B(OH)₂ or hexyl-B(OEthyl)₂ which may be attached via the alkyl or aryl group to a solid support material, such as Agarose;

maltose which binds to maltose binding protein (as well as any other sugar/sugar binding protein pair or more generally to any ligand/ligand binding protein pairs that has properties discussed above);

a hapten, such as dinitrophenyl group, for any antibody where the hapten binds to an anti-hapten antibody that recognizes the hapten, for example the dinitrophenyl group will bind to an anti-dinitrophenyl-IgG;

a ligand which binds to a transition metal, for example, an oligomeric histidine will bind to Ni(II), the transition metal CR may be used in the form of a resin bound chelated transition metal, such as nitrilotriacetic acid-chelated Ni(II) or iminodiacetic acid-chelated Ni(II);

glutathione which binds to glutathione-S-transferase.

Page 13, first full paragraph

A displacement ligand, DL, is optionally used to displace A from CR. Suitable DLs are not typically present in samples unless added. DL should be chemically and enzymatically stable in the sample to be analyzed and should not react with or bind to components (other than CR) in samples or bind non-specifically to reaction vessel walls. DL preferably does not

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undergo peptide-like fragmentation during MS analysis, and its presence in a sample should not significantly suppress the ionization of tagged peptide, substrate or reaction product conjugates.

Page 16, first full paragraph

The requirements discussed above for A, L, PRG, extend to the corresponding segments of A-L-PRG and the reaction products generated with this reagent.

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[Page 16, second full paragraph]

Internal standards, which are appropriately isotopically labeled, may be employed in the methods of this invention to measure absolute quantitative amounts of proteins in samples. Internal standards are of particular use in assays intended to quantitate affinity tagged products of enzymatic reactions. In this application, the internal standard is chemically identical to the tagged enzymatic product generated by the action of the enzyme on the affinity tagged enzyme substrate, but carries isotope labels which may include ^2H , ^{13}C , ^{15}N , ^{17}O , ^{18}O , or ^{34}S , that allow it to be independently detected by MS techniques. Internal standards for use in the method herein to quantitate one or several proteins in a sample are prepared by reaction of affinity labeled protein reactive reagents with a known protein to generate the affinity tagged peptides generated from digestion of the tagged protein. Affinity tagged peptides internal standards are substantially chemically identical to the corresponding affinity tagged peptides generated from digestion of affinity tagged protein, except that they are differentially isotopically labeled to allow their independent detection by MS techniques.

Page 18, third full paragraph

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Protein digestion. The proteins in the sample mixture are digested, typically with trypsin. Alternative proteases are also compatible with the procedure as in fact are chemical fragmentation procedures. In cases in which the preceding steps were performed in the presence of high concentrations of denaturing solubilizing agents the sample mixture is diluted until the denaturant concentration is compatible with the activity of the proteases used. This step may be omitting in the analysis of small proteins;

Page 19, third full paragraph

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Results of applying this method using the biotinylated sulfhydryl reagent and to the quantitative analysis of synthetic peptide samples, to the relative quantitation of the peptides in

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a protein digest and the tandem mass spectral analysis of a derivatized peptide are shown in Fig. 1, Table 1, and Fig. 2, respectively.

Page 22, first full paragraph

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The protein reactive affinity reagent strategy was applied to study differences in steady-state protein expression in the yeast, *S. cerevisiae*, in two non-glucose repressed states (Table 3). Cells were harvested from yeast growing in log-phase utilizing either 2% galactose or 2% ethanol as the carbon source. One-hundred μg of soluble yeast protein from each cell state were labeled independently with the isotopically different affinity tagged reagents. The labeled samples were combined and subjected to the strategy described in Scheme 1. One fiftieth (the equivalent of approximately 2 μg of protein from each cell state) of the sample was analyzed.

Paragraph bridging pages 23 and 24

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The method as applied using a sulfhydryl reactive reagent significantly reduces the complexity of the peptide mixtures because affinity tagged cysteine-containing peptides are selectively isolated. For example, a theoretical tryptic digest of the entire yeast proteome (6113 proteins) produces 344,855 peptides, but only 30,619 of these peptides contain a cysteinyl residue. Thus, the complexity of the mixture is reduced, while protein quantitation and identification are still achieved. The chemical reaction of the sulfhydryl reagent with protein can be performed in the presence of urea, sodium dodecyl sulfate (SDS), salts and other chemicals that do not contain a reactive thiol group. Therefore, proteins can be kept in solution with powerful stabilizing agents until they are enzymatically digested. The sensitivity of the $\mu\text{LC-MS}^n$ system is dependent of the sample quality. In particular, commonly used protein solubilizing agents are poorly compatible or incompatible with MS. Affinity purification of the tagged peptides completely eliminates contaminants incompatible with MS. The quantitation and identification of low abundance proteins by conventional methods requires large amounts (milligrams) of starting protein lysate and involves some type of enrichment for these low abundance proteins. Assays described above, start with about 100 μg of protein and used no fractionation techniques. Of this, approximately 1/50 of the protein was analyzed in a single $\mu\text{LC-MS}^n$ experiment. This system has a limit of detection of 10-20 fmol per peptide (Gygi, S.P. et al. (1999)). For this reason, in the assays described which employ $\mu\text{LC-MS}^n$ only abundant proteins are detected. However, the methods of this invention are compatible with any biochemical, immunological or cell biological fractionation methods that reduce the mixture complexity and enrich for proteins of low abundance while quantitation is maintained. This

method can be redundant in both quantitation and identification if multiple cysteines are detected. There is a dynamic range associated with the ability of the method to quantitate differences in expression levels of affinity tagged peptides which is dependent on both the intensity of the peaks corresponding the peptide pair (or set) and the overall mixture complexity. In addition, this dynamic range will be different for each type of mass spectrometer used. The ion trap was employed in assays described herein because of its ability to collect impressive amounts of sequencing information (thousands of proteins can potentially be identified) in a data-dependent fashion even though it offers a more limited dynamic quantitation range. The dynamic range of the ion trap (based on signal-to-noise ratios) varied depending on the signal intensity of the peptide pair and complexity of the mixture, but differences of up to 100-fold were generally detectable and even larger differences could be determined for more abundant peptides. In addition, protein expression level changes of more than 100-200-fold still identify those proteins as major potential contributors to the phenotypic differences between the two original cell states. The method can be extended to include reactivity toward other functional groups. A small percentage of proteins (8% for *S. cerevisiae*) contain no cysteinyl residues and are therefore missed by analysis using reagents with sulfhydryl group specificity (i.e., thiol group specificity). Affinity tagged reagents with specificities toward functional groups other than sulfhydryl groups will also make cysteine-free proteins susceptible to analysis.

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Page 25, fifth full paragraph

Amino-reactive, differentially isotopically labeled affinity tagged reagents are used to identify the *N*-terminal ion series in MSⁿ spectra. In a preferred version of this application, the peptides to be analyzed are derivatized with a 50:50 mixture of an isotopically light and heavy reagent which is specific for amino groups. Fragmentation of the peptides by CID therefore produces two *N*-terminal ion series which differ in mass precisely by the mass differential of the reagent species used. This application dramatically reduces the difficulty in determining the amino acid sequence of the derivatized peptide.

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Page 28, first full paragraph

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P69SV40T cells (1×10^7) are biotinylated with an isotopically heavy biotin tagged amino reactive reagent and the M12 cells (1×10^7) are biotinylated with a corresponding isotopically light amine reactive biotin tagged amino reactive reagent. IGF-1R is then immunoprecipitated from the combined lysate of both cell lines using an antibody against human IGF-1R and the total mass of immunoprecipitated proteins is digested with trypsin. Trypsin is then neutralized,

e.g., by the addition of inhibitors and tagged peptides are purified by biotin-avidin affinity chromatography. The eluted peptides are analyzed by LC-MS and LC-MSⁿ for peptide quantitation and identification, respectively, as has been described above. Quantitation in this experiment is facilitated by the option to use selective ion monitoring in the MS. In this mode only the masses of tagged peptide ions expected to derive from IGF-1R need be monitored.

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[Page 28, second full paragraph]

The described technique can be applied to compare the differences in relative abundance of cell surface proteins between parental prostate cell line (P69SV40T) and M12 cells to detect and identify those cell surface proteins whose expression level is different in the two cell lines and which may be characteristic of the different cell states. Using the methods described herein, global, relative quantitation of the cell surface proteins in any two or more cell lines can be analyzed to detect and identify those cell surface proteins characteristic of the different cell states. Results can be independently confirmed using procedure such as 1D or 2D gels, if applicable, or quantitative western blotting to confirm quantitation results.

Page 29, heading after second full paragraph

Synthesis of affinity tagged protein reactive reagents that are selective for certain protein groups

[Page 29, third full paragraph]

Synthetic routes of exemplary affinity tagged reagents suitable for use in the methods of this invention are provided in Schemes 2-3 where well-known synthetic techniques are employed in synthesis of the non-deuterated and deuterated reagents.

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[Paragraph bridging pages 29 and 30]

Biotinyl-iodoacetamidyl-4,7,10 trioxatridecanediamine 4 (Scheme 3) consists of a biotin group, a chemically inert spacer capable of being isotopically labeled with stable isotopes and an iodoacetamidyl group, respectively. The biotin group is used for affinity enrichment of peptides derivatized with the reagent, the ethylene glycol linker is differentially isotopically labeled for mass spectral analysis and the iodoacetamidyl group provides specificity of the reagent for sulfhydryl-containing peptides. The reagent can be synthesized in an all hydrogen form (isotopically light form) with 1-20, and preferably 4-8 deuterium atoms in the linker (isotopically heavy forms).

Page 30, second full paragraph

A feature of the method of this invention as applied to enzyme assays is the use of electrospray ionization mass spectrometry (ESI-MS) (Cole et al., 1997) for the simultaneous detection of enzymatic products and chemically identical internal standards, which are distinguished by stable isotope (deuterium) labeling. A second feature is the use of affinity tagged reagents containing an enzyme substrate which when combined with affinity purification provides for facile capture of enzymatic products from crude biological fluids. The affinity tagged reagents are designed to contain a target substrate for an enzyme of interest that is covalently attached to an affinity tag via a linker. Action of the enzyme of interest on the substrate conjugate causes cleavage or other modification that changes its molecular mass (Scheme 4). The change of mass is detected by ESI-MS. The linker and affinity tag used preferably facilitate ionization by ESI, block action of other enzymes in the biological fluid, and allow highly selective capture from the complex matrix for facile purification.

Page 31, first full paragraph

An example of this approach is the design and synthesis of affinity tagged enzyme substrate reagents **1** and **2** (Scheme 5) to simultaneously assay lysosomal β -galactosidase and N-acetyl- α -D-glucosaminidase, respectively. Deficiency of the former enzyme results in one of the lysosomal storage diseases, GM₁-gangliosidosis, a condition that occurs in the population with a frequency of about 1 in 50,000 and leads to early death of affected children. Deficiency of N-acetyl- α -D-glucosaminidase results in the rare lysosomal storage disorder Sanfilippo syndrome type B. This example has been described in Gerber et al. (1999) J. Amer. Chem. Soc. **121**: 1102-1103 which is incorporated by reference herein in its entirety.

Paragraph bridging pages 31 and 32

In addition, the linker is hydrophilic to ensure good water solubility of the substrate conjugate, and it has basic groups which are efficiently protonated by ESI and thus ensure sensitive detection by mass spectrometry. The target carbohydrate substrates are attached to the polyether linker by a β -alanine unit (Scheme 5). The enzymatic product conjugates **3** and **4** are also shown Scheme 5. Conjugates **1** and **2** were prepared as shown in Scheme 5. All reagents were purified to homogeneity by reverse-phase HPLC and characterized by high-field ¹H-NMR and ESI-MS. The substrate was linked to the diamine spacer by Michael addition of the latter onto the p-acryloylamidophenyl glycoside, (Romanowska et al., 1994) and the

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intermediate was coupled with the tetrafluorophenyl ester of N-biotinylsarcosine (Wilbur et al., 1997).

Paragraph bridging pages 33 and 34

The approach described for assaying enzymes using substrate reagents and ESI-MS can be broadly applied. The multiplex technique can be expanded to assay dozens or more enzymes simultaneously in a single reaction, obviating the need for multiple assays to assist in confirming diagnoses of rare disorders. The method can be used to measure several enzymes simultaneously when evaluating the rate of chemical flux through a specific biochemical pathway or for monitoring biochemical signaling pathways. The affinity tag-capture reagent method for isolation of affinity tagged reaction products and substrates from complex mixtures is technically simple and can be readily automated, particular when biotin-streptavidin is employed. Because of the high sensitivity of the ESI-MS detection employed, which requires only sub-microgram quantities of the substrate reagents per assay, the synthesis of several hundred substrate reagents on a low-gram scale becomes practical and economical. Since most enzyme active sites are exposed to solvent, it is possible to attach an affinity tagged linker to most enzyme substrates while preserving enzymatic activity. Scheme 6 provides the structures of several additional enzyme substrates, suitable for use in this method, indicating by arrows allowable positions for tag attachment sites. Allowable tag sites for additional enzyme substrates can be determined by review of X-ray crystal structures of enzyme-substrate or enzyme-substrate analog structures. Using a standard computer graphics program, available X-ray data and by attaching an extended chain butyl group (as a model for the affinity tagged linker) to potential tag attachment sites, suitable attachment sites that show there are no enzyme-atoms in van der Waals overlap with the model tag can be predicted.

Page 34, second full paragraph

Table 4 provides exemplary enzymes that are associated with certain birth defects or disease states. These enzymes can be assayed by the methods described herein.

Page 36, first full paragraph

The synthesis of a biotinylated dolichol₁₀-substrate conjugate containing a sarcosinyl linker (B-S-Dol₁₀-P) is shown in Scheme 9. Protected citronellol (R = *t*-BuSiMe₂) is regioselectively oxidized at the terminal allylic methyl group (McMurry and Kocovsky, 1984), and the allylic alcohol is coupled with biotinylsarcosine active ester (R = CH₃). The citronellol 1-

hydroxy group is subsequently deprotected and phosphorylated with POCl_3 (Rush and Wachter, 1995). In a parallel synthesis, d_5 -sarcosine, $\text{CD}_3\text{NHCD}_2\text{COOH}$, is used to prepare the isotopically labeled (heavy) reagent for use as an internal standard. d_5 -Sarcosine is readily prepared from commercially available materials (BrCD_2COOD and CD_3NH_2) using standard synthetic techniques.

Paragraph bridging pages 36 and 37

CDGS Type II results from defective GlcNAc transferase II (GlcNAc-T II) which transfers GlcNAc from UDP-GlcNAc to the 2-position of a mannose residue in the intermediate branched oligosaccharide (the Core Region) in the process of building up the disialobiantennary chain (Scheme 10) (Schachter, 1986, Brockhausen et al, 1989). GlcNAc transferase II is one of the six known enzymes that mediate highly regiospecific glycosylation of the mannose residues in the Core Region. The Core Region is anchored at the reducing end to chitobiosylasparagine, where the asparagine residue is part of the peptide chain of the glycosylated protein. The latter structure unit in the substrate can be replaced by a hydrophobic chain without loss of enzyme activity (Kaur et al, 1991). Thus, the substrate conjugate for CDGS Type II is assembled by linking an affinity-labeled linker group to the reducing end of chitobiosylasparagine. However, the latter structure unit in the substrate can be replaced by a hydrophobic chain without loss of enzyme activity (Kaur et al, 1991). For example, commercially available α -D-manno-pyranosylphenylisothiocyanate can be coupled to a biotin-labeled linker and the 5,6-hydroxyls are selectively protected as illustrated in Scheme 11 (Paulsen and Meinjohanns, 1992). Coupling of the equatorial 3-OH with per-O-acetylmannosyl-1-trichloroacetamide (Paulsen et al, 1993) will provide a disaccharide conjugate (Scheme 12). If a minor amount of coupling occurs at the axial 2-OH group the products can be separated by HPLC. After deprotection, the primary 6-OH is coupled with a second equivalent of per-O-acetylmannosyl-1-trichloroacetamide to yield the Core Region conjugate. Deprotection of the O-acetyl groups yields the substrate conjugate for GlcNAc transferase I which can be converted to the GlcNAc-T II substrate by enzymatic glycosyl transfer using a Triton X-100 rabbit liver extract, a reaction that has been carried out on a preparative scale (Kaur et al. 1981).

Page 39, third full paragraph

The total enzyme reaction volume is 20 - 30 mL. The substrate stock solutions are maintained at concentrations of 3mM (SFB) and 2mM (GM1). These concentrations were measured by $^1\text{H-NMR}$ signal integration versus an internal standard (formamide proton of

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DMF). Final concentration of substrates is 0.3 and 0.2 mM, respectively. A volume of reaction buffer (e.g. 200mM sodium citrate, pH 4.5) equal to the difference of the substrate addition (2-3 mL) plus sufficient cell sample volume to equal 50 - 75mcg total protein from 20-30 mL is added to a 0.5 mL Eppendorf tube, followed by substrate. The sample is cooled on ice, and patient cell sample is added. The reaction is initiated by incubation at 37°C.

Page 40, fifth full paragraph

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Patient skin fibroblasts were obtained as frozen pellets, and stored at -20°C until use. Two GM1 affected samples and six normal controls were analyzed.

Page 43, first full paragraph

1. 2,3,5,6-Tetrafluorophenyl trifluoroacetate (1) 25g (0.15mol) 2,3,5,6-tetrafluorophenol, 35 mL (0.2mol) trifluoroacetic anhydride and 0.5 mL boron trifluoride etherate were refluxed for 18 hours under argon atmosphere. Trifluoroacetic anhydride and trifluoroacetic acid were removed by distillation at room temperature. The trifluoroacetic anhydride fraction was returned to the mixture, and the reaction was refluxed for 24 hours. This was repeated twice. After final distillation at room temperature, the desired product 1 was distilled at reduced pressure (62°C/45mmHg) to produce a colorless liquid (30g, 82%). ¹H-NMR. (Gamper, H. B., 1993).

2. Biotin-2,3,5,6-tetrafluorophenyl ester (2) A 2.5g (10.3mmol) quantity of d-biotin in 20 mL anhydrous DMF under argon atmosphere was warmed to 60°C with stirring to effect dissolution. 1.7 mL (12.5mmol) triethylamine was added, followed by 3.4g (12.5mmol) 1. The mixture was stirred for 2 hours, after which the solvent was removed by rotary evaporation. The resultant semi-solid was triturated with 15 mL ether twice to produce a white solid (2.6g, 65%). ¹H-NMR. (Wilbur, D. S., et al., 1997).

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3. N-methylglycylbiotinamide-methyl ester (3) A 2.5g (6.4mmol) quantity of biotin tetrafluorophenyl ester in 30 mL anhydrous DMF under argon atmosphere was added to a mixture of 1.1g (7.7mmol) N-methylglycine methyl ester hydrochloride dissolved in 10 mL anhydrous DMF and 1.25 mL (9.0 mmol) triethylamine. The reaction mixture was stirred at room temperature for 2 hours, then the solvent was removed by rotary evaporation. The residue was extracted with chloroform (2x100 mL), washed with water (2x20 mL), and dried with anhydrous sodium sulfate. The solvent was removed under vacuum to yield 2.1g (98 %) of methyl ester of N-methylglycine biotinamide as an oil. ¹H-NMR. (Wilbur, D. S., et al., 1997).

Paragraph bridging pages 44 and 45

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7. GM1 substrate conjugate of 4 and 6 (7) A 2.5mg (7.4mcmol) quantity of 4 was dissolved in 1.5 mL anhydrous DMF with stirring, under argon atmosphere. 5 mL triethylamine was added, followed by 2.3mg (8.8mcmol) 1. The formation of active ester was monitored by silica TLC (5:1 CHCl₃/CH₃OH, R_f 0.5, UV) by briefly drying the spotted TLC plate with a stream of air. After 25 minutes, the mixture was added to 3.2mg (5.9mcmol) 6 in 1 mL anhydrous DMF. After 2 hours, the solvent was removed by vacuum centrifugation and the final product was purified by reverse-phase HPLC (Vydac C-18 prep-scale column, 6 mL/min. Mobile phase: H₂O (0.08%TFA)/ ACN (0.08%TFA)). Yield 4.6 mg. (For analogous chemistry, see Wilbur, D. S., et al., 1997).

Page 46, second full paragraph

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12. GM1 internal standard conjugate (12) 1.8mg 11 was added to 2 mL of 100mM Tris/10mM MgCl₂, pH 7.3 buffer with stirring. 15 units recombinant β -D-galactosidase (Sigma) was added, and after 12 hours the mixture was purified by reverse-phase HPLC (Vydac C-18 prep-scale column, 6 mL/min. Mobile phase: H₂O (0.08%TFA)/ACN (0.08%TFA)). Yield 1.5 mg.

Page 51, third full paragraph

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23. SFB internal standard conjugate (29) 1.2mg 28 was added to 2 mL of 100mM Tris/10mM MgCl₂, pH 7.3 buffer with stirring. 15 units recombinant β -D-galactosidase (Sigma) were added, and after 12 hours the mixture was purified by reverse-phase HPLC (Vydac C-18 prep-scale column, 6 mL/min. Mobile phase: H₂O (0.08%TFA)/ACN (0.08%TFA)). Yield 0.7 mg.

Page 56, first full paragraph

A30
An automated LC-MS/MS system for the identification of proteins by their amino acid sequence has been developed. A schematic representation is shown in Fig. 7. The system, which consists of an autosampler, a capillary HPLC system connected on-line to an ESI triple quadrupole MS/MS instrument and a data system is operated in the following way: Proteins (typically separated by 1D or 2D gel electrophoresis) are cleaved with a specific protease, usually trypsin. the resulting cleavage fragments are placed in an autosampler. Every 37 minutes the autosampler injects one sample into the HPLC system and the peptides are separated by capillary reverse-phase chromatography. As separated peptides elute from the chromatography column, they are ionized by the ESI process, enter the MS and the mass to

charge ratio (m/z) is measured. Any peptide ion whose intensity exceeds a predetermined intensity threshold is automatically selected by the instrument and collided in the collision cell with inert gas. These collisions result in peptide fragmentation, primarily at the bonds of the peptide backbone (collision induced dissociation, CID). The masses of the CID fragments are measured and recorded in the data system. The CID spectrum of a peptide contains sufficient information to identify the protein by searching sequence databases with the uninterpreted MS/MS spectra. This is accomplished with the Sequest program. The program identifies each peptide in a sequence database which has the same mass as the peptide that was selected in the MS for CID and predicts the MS/MS spectrum for each one of the isobaric peptides. By matching the experimentally determined CID spectrum with computer generated theoretical CID spectra, the protein from which the observed peptide originated is identified. The system is capable of analyzing protein samples in a fully automated fashion at a pace of less than 40 min. per sample. Since each peptide represents an independent protein identification and usually multiple peptides are derived from one protein, protein identification by this method is redundant and tolerant to proteins co-migrating in a gel. The system is well suited for the detection and characterization of modified residues within polypeptide chains. The LC-MS/MS technique and automated analysis of the generated CID spectra can be used for the methods of this invention.

Page 57, first full paragraph

Protein identification by this method is based on the same principle as described above, except that peptide separation and ionization are performed at significantly higher sensitivity. Fig. 8 shows a schematic representation of the key design elements. The design of the system and its mode of operation have been published. Peptides derived from protein digests are concentrated by SPE, separated by CE and analyzed by ESI-MS/MS. The resulting uninterpreted CID spectra are used to search sequence databases with the Sequest software system. The SPE extraction device is a small reversed-phase chromatography column of the dimensions 0.18 x 1 mm which is directly packed in a fused silica separation capillary. Peptides contained in a sample solution are adsorbed and concentrated on the SPE device, eluted in an estimated 100 - 300 nl of organic solvent and further concentrated by electrophoretic stacking and/or isotachopheresis to an estimated volume of 5-30 nl. The peptides are then separated by CE in a 20 μ m or 50 μ m i.d. capillary and directly ionized by ESI as they leave the capillary (see reference 13 for design of the microspray ionization source). With this system, peptide masses can be determined at a sensitivity of 660 attomoles (approx. 500 fg for a 20 residue peptide) at a concentration limit of 33 amol/ μ l and proteins can be identified by the CID spectra of

automatically selected peptides at less than 10 fmol (0.5 ng for a protein of 50 kDa) of sample at a concentration limit of less than 300 amol/ μ l. This technique is used for the analysis at very high sensitivity of the peptide samples generated by the experiments. It has also been demonstrated that the analysis time available for automated CID experiments can be significantly extended by data-dependent modulation of the CE voltage. If several peptide ions are detected coincidentally in the MS, the CE voltage is automatically dropped. This results in a reduction of the electroosmotic flow out of the capillary and therefore in an extension of the time period available for selecting peptide ions for CID. The net effect of this peak parking technique is an extension of the dynamic range of the technique because the increased time available is used for CID of ions with a low ion current. Once all the peptide ions are analyzed, electrophoresis is automatically reaccelerated by increasing the CE voltage to the original value.

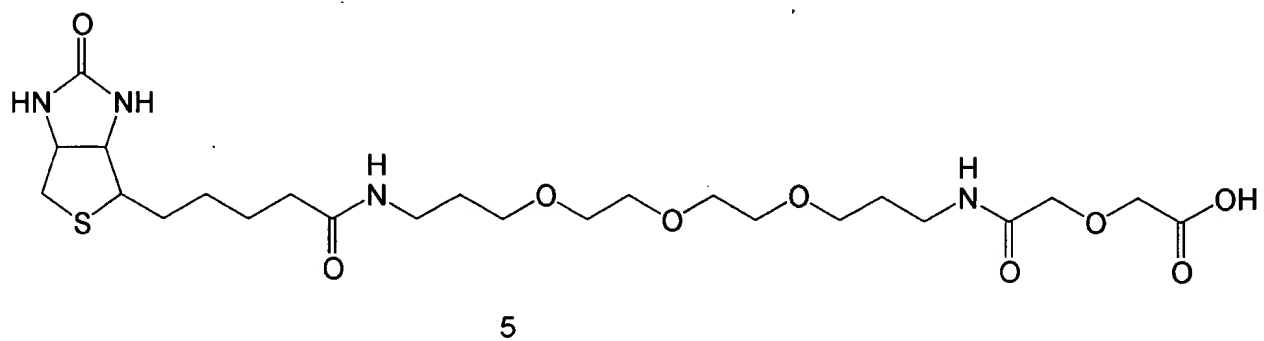
Page 58, replace Table 1 with the following

TABLE 1. Relative, redundant quantitation of α -lactalbumin abundance (after mixing with known amount of the same protein with cysteines modified with isotopically heavy biotinylating reagent)

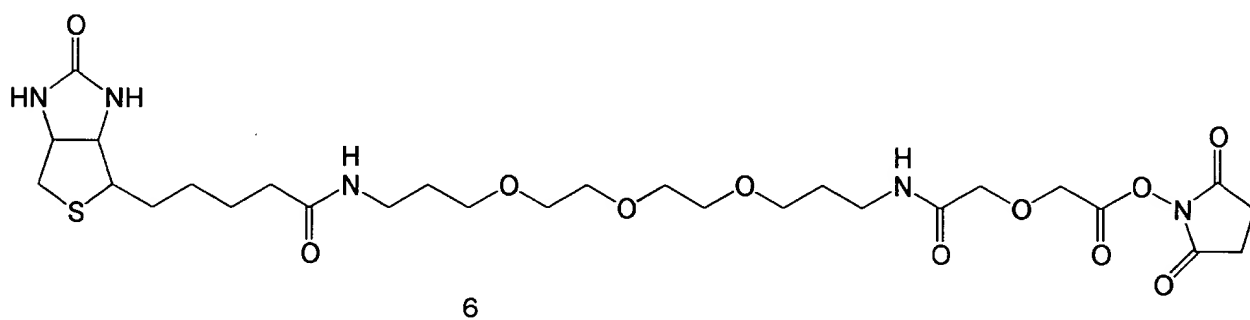
Peptide #	<i>m/z</i> (light)	Charge state	Peptide Sequence	Ratio (heavy:light)
1	518.4	2+	(K) IWCK	2.70
2	568.4	2+	(K) ALCSEK (SEQ ID NO:2)	2.68
3	570.4	2+	(K) CEVFR (SEQ ID NO:3)	2.9
4	760.5	2+	(K) LDQWLCEK (SEQ ID NO:4)	2.82
5	710.1	3+	(K) FLDDDLTDDIMCVK (SEQ ID NO:5)	2.88
6	954.2	3+	(K) DDQNPSSNICNISCDK (SEQ ID NO:6)	2.9
7	1286.9	4+	(K) GYGGVSLPEWCTTFHTSGYDT QAIVQNNDSTEYGLFQINNKK (SEQ ID NO: 7)	NA ^a

^a Isotope ratio was not analyzed because on a 4⁺ peptide the isotope patterns were highly overlapping due to differences of only 2 amu between heavy and light ions.

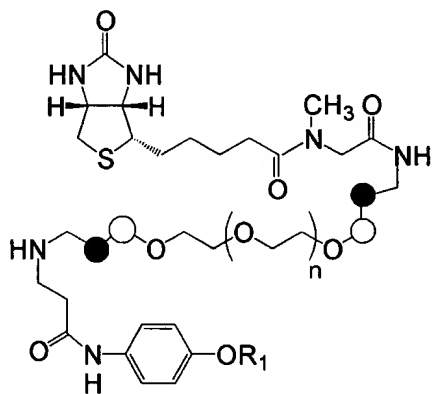
Page 76, replace Scheme 3, structure 5 with the following



Page 76, replace Scheme 3, structure 6 with the following

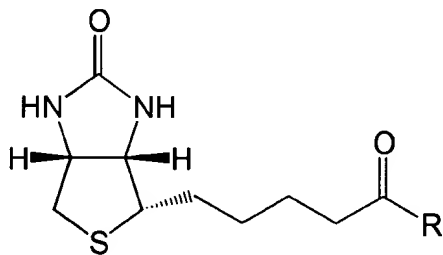


Page 77, replace the last structure in the reaction in Scheme 5 with the following

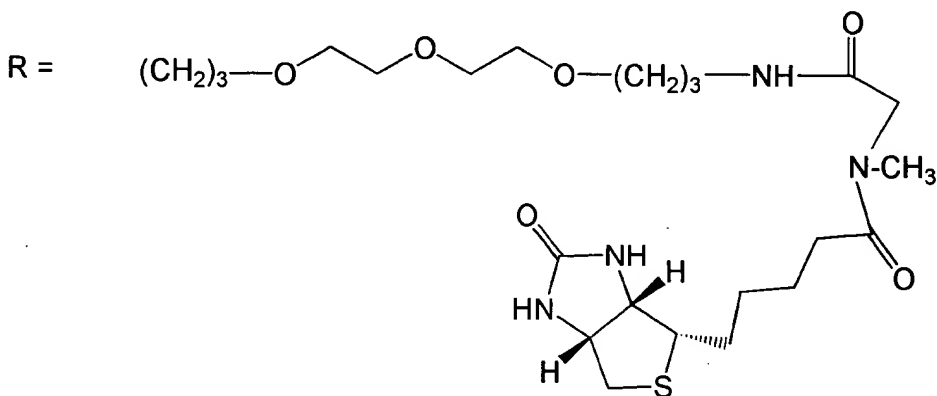


Page 83, replace the chemical structure containing the "R" group in Scheme 14 with the following

A35

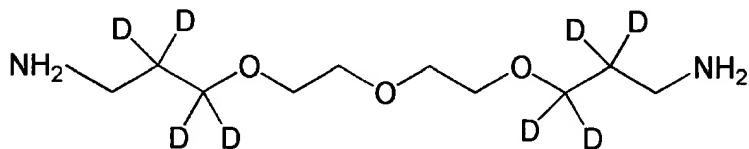


Page 84, replace Scheme 15, structure 7 with the following



[Page 84, replace Scheme 15, structure 9 with the following]

A36

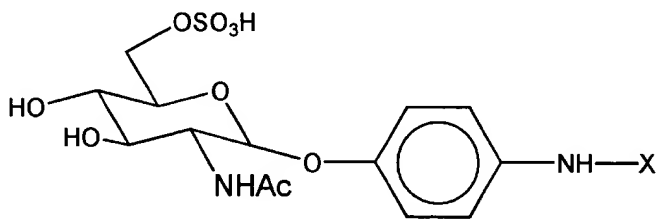


[illegible]OC1=CC=C(C=C1)NC(=O)CCNC(CD)(CD)C(=O)OCCOCCOCCOCC(=O)NCC(=O)N(C)C

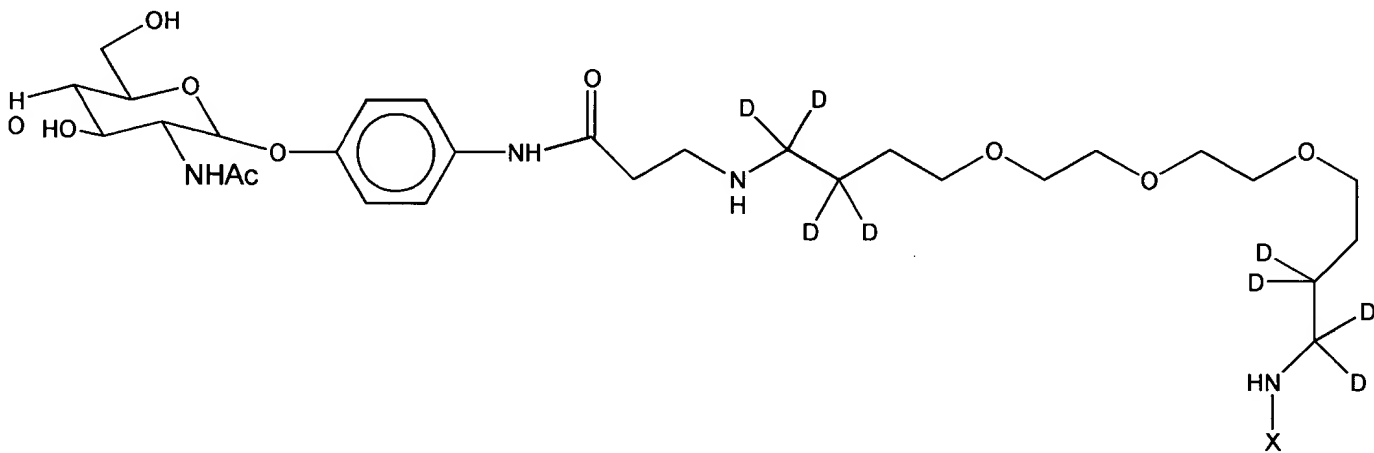
Page 87, replace Scheme 18, structure 24 with the following



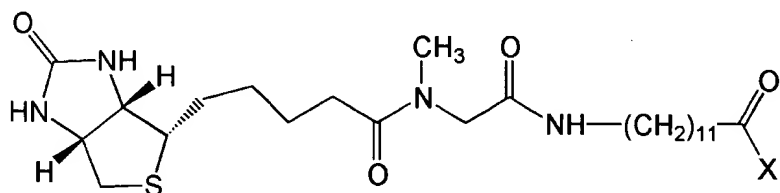
Page 89, replace the first structure in Scheme 20 with the following



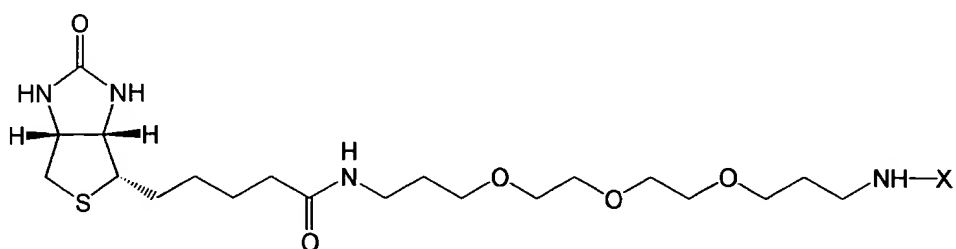
Page 90, replace the chemical structure containing X in Scheme 21 with the following



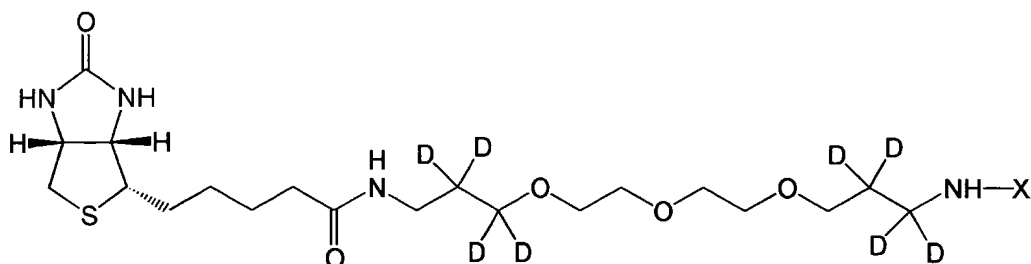
Page 91, replace the first chemical structure in Scheme 22 with the following



Page 92, replace the first chemical structure containing "X" in Scheme 23 with the following



Q42 [Page 92, replace the second chemical structure containing "X" in Scheme 23 with the following]



In the Drawings

Enclosed are red-lined copies of proposed drawing changes to Figures 4B, 5B and 5C.

Figures 5B and 5C were amended to add "G" to the sequence ID for each figure.

Figure 4B was amended to change "L", first occurrence, in peptide #3, to "I".